We claim:

1. A method of determining the clinical outcome of a subject with a cancer using a Genomic Damage Fraction comprising,

a. determining the relative change in quantity of nucleic acids between cancerous cells and non-cancerous cells of said subject;

b. determining the Genomic Damage Fraction from the results of step (a)

c. determining the prognosis of said subject according to said subject's GDF, where a GDF greater than a predetermined GDF is indicative of a first clinical outcome, and a GDF lesser than a predetermined GDF is indicative of a second clinical outcome.

2. The method of claim 1, wherein the relative change in quantity of nucleic acids is determined using AP-PCR DNA fingerprinting.

3. The method of claim 1, wherein said first clinical outcome is increased risk.

4. The method of claim 1, wherein said second clinical outcome is decreased risk.

5. The method of claim 1, wherein the relative change in nucleic acids is determined by the number of qualitative and/or quantitative changes in the DNA fingerprint bands present in the cancerous cells as compared with the normal cells.

6. The method of claim 5, wherein the relative change in nucleic acids is determined by the number of quantitative changes in the DNA fingerprint bands.

7. The method of claim 5, wherein the relative change in nucleic acids is determined by the number of qualitative changes in the DNA fingerprint bands.

8. The method of claim 5, wherein the relative change in nucleic acids is determined by the number of quantitative and qualitative changes in the DNA fingerprint bands.

9. The method of claim 1, wherein the relative change in nucleic acids is a gain in quantity in nucleic acids.

10. The method of claim 1, wherein the relative change in nucleic acids is the combination of gain and loss in quantity in nucleic acids.

11. The method of claim 1, wherein the relative change in nucleic acids is a gain in quantity in nucleic acids.

12. The method of claim 1, wherein the subject with cancer has colorectal cancer.

13. A method of determining the clinical outcome of a subject with a cancer comprising,

a. generating the AP-PCR DNA fingerprint of non-cancerous cells from said subject;

b. generating the AP-PCR DNA fingerprint of primary cancer cells from said subject;

c. generating the AP-PCR DNA fingerprint of metastatic cancer cells from said subject; and

d. identifying chromosomal regions from AP-PCR DNA fingerprint data of steps (a), (b) and (c) wherein the occurrence of gains or losses of nucleic acids in certain chromosomal regions is prognostic of the clinical outcome for said subject.

14. The method of claim 13, wherein the gain and loss of nucleic acids is significantly different in metastatic cancer cells as compared to primary cancer cells.

15. The method of claim 13, wherein said chromosomal region is determined by a band of chromosome 4 obtained using the Blue primer (SEQ ID No: 1).

16. The method of claim 15, wherein said band is band N from the DNA fingerprint generated with the Blue primer (SEQ ID. NO:1).

17. A method of determining the clinical outcome of a subject with a cancer comprising,

a. generating the AP-PCR DNA fingerprint of non-cancerous cells from said subject;

b. generating the AP-PCR DNA fingerprint of primary cancer cells from said subject;

c. identifying chromosomal regions from AP-PCR DNA fingerprint data of steps (a) and (b), where gains or losses of nucleic acids occur; and

d. comparing said AP-PCR DNA fingerprints of chromosomes 1, 4, 6, 8, 9, and 13 from step a and step b wherein presence of gain or loss of nucleic acids in certain chromosomal regions is prognostic of the clinical outcome for said subject.

18. The method of claim 17 wherein said chromosomal region that is determined by band N of chromosome 4 from the BLUE primer (SEQ ID NO: 1) fingerprint is prognostic of the clinical outcome for said subject.

19. A method of predicting a clinical outcome of a subject with cancer using an amplotype from said subject comprising,

a. locating chromosomal regions that have gained and lost nucleic acids using AP-PCR DNA fingerprinting;

b. identifying said chromosomal regions that have lost nucleic acids; and

c. identifying said chromosomal regions that have gained nucleic acids;

wherein the combination of gains and losses according to chromosomal regions are prognostic of the clinical outcome for subject with cancer.

20. The method of claim 19, wherein the results of step (b) and step (c) are displayed where said gains and losses of nucleic acids are listed according to the chromosomal regions where they occur, wherein the combination of gains and losses according to chromosomal regions are prognostic of the clinical outcome for subject with cancer.

21. A method of identifying a genomic region relevant for a cancer in a subject having said cancer comprising,

(a) generating the AP-PCR DNA fingerprint of non-cancerous cells, primary cancer, and metastatic tumor cells from said subject; and

(b) identifying said genomic regions from AP-PCR DNA fingerprint data of step (a), showing gains and losses of nucleic acids is certain genomic regions thereby identifying a genomic region linked to a cancer gene.

22. The method of claim 21, wherein said cancer is colorectal cancer.

23. The method of claim 21, wherein the said AP-PCR DNA fingerprint is generated with the Blue primer (SEQ ID NO: 1).